

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 11:45:50 ; Search time 6433 Seconds  
(without alignments)  
10801.303 Million cell updates/sec

Title: US-10-790-224A-19

Perfect score: 1434

Sequence: 1 gtggcgttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result | Query  |       |        |    | Description |                   |
|--------|--------|-------|--------|----|-------------|-------------------|
| No.    | Score  | Match | Length | DB | ID          | Description       |
| <hr/>  |        |       |        |    |             |                   |
| 1      | 1434   | 100.0 | 1434   | 6  | CQ871075    | CQ871075 Sequence |
| 2      | 1434   | 100.0 | 2500   | 6  | CQ817721    | CQ817721 Sequence |
| 3      | 1424.4 | 99.3  | 1554   | 6  | AX063815    | AX063815 Sequence |

|    |        |       |        |        |          |                    |                    |
|----|--------|-------|--------|--------|----------|--------------------|--------------------|
| 4  | 1424.4 | 99.3  | 3686   | 1      | CGGLNA   | Y13221 Corynebacte |                    |
| 5  | 1424.4 | 99.3  | 326150 | 1      | AP005281 | AP005281 Corynebac |                    |
| 6  | 1424.4 | 99.3  | 349575 | 1      | BX927154 | BX927154 Corynebac |                    |
| 7  | 1424.4 | 99.3  | 349980 | 6      | AX127150 | AX127150 Sequence  |                    |
| 8  | 1421.4 | 99.1  | 1431   | 6      | BD165686 | BD165686 Novel pol |                    |
| 9  | 1421.4 | 99.1  | 1431   | 6      | AX123569 | AX123569 Sequence  |                    |
| 10 | 1397.2 | 97.4  | 1690   | 1      | AF005635 | AF005635 Corynebac |                    |
| 11 | 1098.6 | 76.6  | 306650 | 1      | AP005221 | AP005221 Corynebac |                    |
| 12 | 936.2  | 65.3  | 348408 | 1      | BX248358 | BX248358 Corynebac |                    |
| c  | 13     | 816.2 | 56.9   | 110000 | 1        | AP006618_18        | Continuation (19 o |
|    | 14     | 784.2 | 54.7   | 2216   | 1        | AY008693           | AY008693 Mycobacte |
|    | 15     | 752.8 | 52.5   | 313846 | 1        | AE017234           | AE017234 Mycobacte |
|    | 16     | 705.8 | 49.2   | 1437   | 1        | AF458290           | AF458290 Mycobacte |
|    | 17     | 705.8 | 49.2   | 1437   | 6        | AX935596           | AX935596 Sequence  |
|    | 18     | 705.8 | 49.2   | 1872   | 1        | MTU87280           | U87280 Mycobacteri |
|    | 19     | 705.8 | 49.2   | 38793  | 1        | MSGB27CS           | L78817 Mycobacteri |
|    | 20     | 705.8 | 49.2   | 110000 | 1        | AE000516_24        | Continuation (25 o |
|    | 21     | 705.8 | 49.2   | 306050 | 1        | BX248341           | BX248341 Mycobacte |
|    | 22     | 705.8 | 49.2   | 348247 | 1        | BX842579           | BX842579 Mycobacte |
|    | 23     | 705.8 | 49.2   | 348450 | 1        | MLEPRTN4           | AL583920 Mycobacte |
|    | 24     | 704.2 | 49.1   | 1437   | 6        | AR361070           | AR361070 Sequence  |
|    | 25     | 704.2 | 49.1   | 1437   | 6        | BD064140           | BD064140 Abundant  |
|    | 26     | 693.2 | 48.3   | 12641  | 1        | AE014731           | AE014731 Bifidobac |
|    | 27     | 693.2 | 48.3   | 349980 | 6        | AX492785           | AX492785 Sequence  |
|    | 28     | 693.2 | 48.3   | 349980 | 6        | AX553952           | AX553952 Sequence  |
|    | 29     | 673.2 | 46.9   | 2280   | 1        | STMGLNA            | M23172 Streptomyce |
|    | 30     | 673.2 | 46.9   | 321250 | 1        | SCO939111          | AL939111 Streptomy |
|    | 31     | 665.8 | 46.4   | 2600   | 1        | AF050112           | AF050112 Amycolato |
| c  | 32     | 663.2 | 46.2   | 299925 | 1        | AP005045           | AP005045 Streptomy |
|    | 33     | 661.6 | 46.1   | 1889   | 1        | SRU58138           | U58138 Streptomyce |
| c  | 34     | 658.4 | 45.9   | 110000 | 1        | AE016822_10        | Continuation (11 o |
|    | 35     | 654   | 45.6   | 1410   | 1        | SVGLNAIA           | X70924 S.viridochr |
|    | 36     | 581.6 | 40.6   | 34088  | 6        | CQ363778           | CQ363778 Sequence  |
| c  | 37     | 581.6 | 40.6   | 110000 | 1        | AE017283_07        | Continuation (8 of |
|    | 38     | 578.4 | 40.3   | 1719   | 1        | FRAGLNAA           | L10631 Frankia aln |
| c  | 39     | 538.8 | 37.6   | 110000 | 1        | AE017180_19        | Continuation (20 o |
| c  | 40     | 538.8 | 37.6   | 110000 | 1        | AE017180_20        | Continuation (21 o |
|    | 41     | 533.8 | 37.2   | 299700 | 1        | AP006571           | AP006571 Gloeobact |
| c  | 42     | 524.4 | 36.6   | 197050 | 1        | AL646081           | AL646081 Ralstonia |
|    | 43     | 492.6 | 34.4   | 1910   | 1        | AZSGLN             | M26107 A.brasilens |
|    | 44     | 492.4 | 34.3   | 300600 | 1        | AP005952           | AP005952 Bradyrhiz |
|    | 45     | 490.2 | 34.2   | 1950   | 1        | AVIGLNA            | M57275 A.vinelandi |

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 08:55:40 ; Search time 840 Seconds  
(without alignments)  
10105.844 Million cell updates/sec

Title: US-10-790-224A-19

Perfect score: 1434

Sequence: 1 gtggcgttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | Score  | Query |        |             | Description        |
|---------------|--------|-------|--------|-------------|--------------------|
|               |        | Match | Length | DB ID       |                    |
| 1             | 1434   | 100.0 | 1434   | 13 ADS73713 | Ads73713 B. lactof |
| 2             | 1434   | 100.0 | 2500   | 12 ADP87711 | Adp87711 Brevibact |
| 3             | 1424.4 | 99.3  | 1554   | 4 AAF71801  | Aaf71801 Corynebac |
| 4             | 1424.4 | 99.3  | 349980 | 5 AAH68531  | Aah68531 C.glutami |

|    |        |       |        |      |             |                    |                    |
|----|--------|-------|--------|------|-------------|--------------------|--------------------|
| 5  | 1421.4 | 99.1  | 1431   | 5    | AAH68450    | Aah68450 C glutami |                    |
| 6  | 933.2  | 65.1  | 1434   | 8    | ACA29721    | Aca29721 Prokaryot |                    |
| 7  | 705.8  | 49.2  | 1437   | 2    | AAV42598    | Aav42598 M. tuberc |                    |
| 8  | 705.8  | 49.2  | 1437   | 2    | AAV29069    | Aav29069 Mycobacte |                    |
| 9  | 705.8  | 49.2  | 1437   | 10   | ADF18437    | Adf18437 Mycobacte |                    |
| 10 | 705.8  | 49.2  | 38110  | 8    | AAL53730    | Aal53730 Ribonucle |                    |
| 11 | 705.8  | 49.2  | 38110  | 8    | AAD49662    | Aad49662 Mycobacte |                    |
| 12 | 705.8  | 49.2  | 110000 | 4    | AAI99682_24 | Continuation (25 o |                    |
| 13 | 705.8  | 49.2  | 110000 | 4    | AAI99683_24 | Continuation (25 o |                    |
| 14 | 704.2  | 49.1  | 1437   | 2    | AAT71594    | Aat71594 Mycobacte |                    |
| 15 | 704.2  | 49.1  | 1437   | 10   | AAD59703    | Aad59703 M. tuberc |                    |
| 16 | 693.2  | 48.3  | 349980 | 6    | ABQ81847    | Abq81847 Bifidobac |                    |
| 17 | 581.6  | 40.6  | 34088  | 4    | AAS59566    | Aas59566 Propionib |                    |
| 18 | 581.6  | 40.6  | 34088  | 8    | ACF64495    | Acf64495 Propionib |                    |
| 19 | 483.8  | 33.7  | 1410   | 4    | AAS54353    | Aas54353 Pseudomon |                    |
| 20 | 483.8  | 33.7  | 1410   | 8    | ACA42733    | Aca42733 Prokaryot |                    |
| 21 | 481    | 33.5  | 1446   | 11   | ABD17636    | Abd17636 Pseudomon |                    |
| c  | 22     | 479.6 | 33.4   | 1500 | 11          | ABD17747           | Abd17747 Pseudomon |
|    | 23     | 460.2 | 32.1   | 1497 | 8           | ACA27260           | Aca27260 Prokaryot |
|    | 24     | 458.8 | 32.0   | 1404 | 8           | ACA43893           | Aca43893 Prokaryot |
|    | 25     | 456   | 31.8   | 1413 | 8           | ACA23419           | Aca23419 Prokaryot |
|    | 26     | 449.6 | 31.4   | 1413 | 8           | ACA25929           | Aca25929 Prokaryot |
|    | 27     | 446.2 | 31.1   | 1407 | 8           | ACA31947           | Aca31947 Prokaryot |
|    | 28     | 434.8 | 30.3   | 1404 | 8           | ACA45511           | Aca45511 Prokaryot |
|    | 29     | 423.6 | 29.5   | 1410 | 8           | ACA53509           | Aca53509 Prokaryot |
|    | 30     | 419   | 29.2   | 1407 | 8           | ACA35419           | Aca35419 Prokaryot |
|    | 31     | 415.2 | 29.0   | 1431 | 11          | ACH99251           | Ach99251 Klebsiell |
| c  | 32     | 415.2 | 29.0   | 1488 | 11          | ACH99262           | Ach99262 Klebsiell |
|    | 33     | 398   | 27.8   | 1410 | 8           | ACA53962           | Aca53962 Prokaryot |
|    | 34     | 392   | 27.3   | 1344 | 8           | ACA25130           | Aca25130 Prokaryot |
|    | 35     | 391.8 | 27.3   | 1410 | 4           | AAS52684           | Aas52684 E. coli D |
|    | 36     | 391.8 | 27.3   | 1410 | 8           | ACA32714           | Aca32714 Prokaryot |
|    | 37     | 391.8 | 27.3   | 1410 | 10          | ADI53076           | Adi53076 E. coli g |
|    | 38     | 391.8 | 27.3   | 1410 | 12          | ADI38943           | Adi38943 Glutamine |
|    | 39     | 391.2 | 27.3   | 1410 | 4           | AAS56054           | Aas56054 Salmonell |
|    | 40     | 391.2 | 27.3   | 1410 | 8           | ACA52006           | Aca52006 Prokaryot |
|    | 41     | 382.2 | 26.7   | 1419 | 8           | ACA42021           | Aca42021 Prokaryot |
| c  | 42     | 375.8 | 26.2   | 1530 | 10          | ABZ41832           | Abz41832 N. gonorr |
|    | 43     | 375   | 26.2   | 1409 | 8           | ACA49431           | Aca49431 Prokaryot |
|    | 44     | 374.8 | 26.1   | 1533 | 8           | ACA41116           | Aca41116 Prokaryot |
|    | 45     | 374.8 | 26.1   | 1572 | 10          | ABZ41834           | Abz41834 N. gonorr |

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 10:08:30 ; Search time 269 Seconds  
(without alignments)  
8722.754 Million cell updates/sec

Title: US-10-790-224A-19

Perfect score: 1434

Sequence: 1 gtggcgttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query |       |       |         |       | Description          |
|--------|-------|-------|-------|---------|-------|----------------------|
|        | No.   | Score | Match | Length  | DB ID |                      |
|        | 1     | 705.8 | 49.2  | 1437    | 3     | US-08-724-814-15     |
|        | 2     | 705.8 | 49.2  | 4403765 | 3     | US-09-103-840A-2     |
|        | 3     | 705.8 | 49.2  | 4411529 | 3     | US-09-103-840A-1     |
|        | 4     | 704.2 | 49.1  | 1437    | 4     | US-09-157-689-93     |
|        | 5     | 481   | 33.5  | 1446    | 4     | US-09-252-991A-16240 |
| c      | 6     | 479.6 | 33.4  | 1500    | 4     | US-09-252-991A-16351 |
|        | 7     | 415.2 | 29.0  | 1431    | 4     | US-09-489-039A-5046  |
| c      | 8     | 415.2 | 29.0  | 1488    | 4     | US-09-489-039A-5057  |
|        | 9     | 335   | 23.4  | 1470    | 4     | US-09-328-352-237    |
|        | 10    | 328.6 | 22.9  | 948     | 4     | US-09-252-991A-16139 |
|        | 11    | 289   | 20.2  | 1482    | 4     | US-09-543-681A-2582  |

|      |       |      |         |   |                      |                    |
|------|-------|------|---------|---|----------------------|--------------------|
| 12   | 277.6 | 19.4 | 1830121 | 4 | US-09-557-884-1      | Sequence 1, Appli  |
| 13   | 277.6 | 19.4 | 1830121 | 4 | US-09-643-990A-1     | Sequence 1, Appli  |
| 14   | 247.4 | 17.3 | 1431    | 4 | US-09-540-236-486    | Sequence 486, App  |
| 15   | 244.2 | 17.0 | 65792   | 4 | US-09-596-002-31     | Sequence 31, Appli |
| c 16 | 170.8 | 11.9 | 1664976 | 4 | US-08-916-421B-1     | Sequence 1, Appli  |
| c 17 | 170.8 | 11.9 | 1664976 | 4 | US-09-692-570-1      | Sequence 1, Appli  |
| 18   | 150   | 10.5 | 1341    | 3 | US-08-724-814-19     | Sequence 19, Appli |
| c 19 | 148.4 | 10.3 | 4403765 | 3 | US-09-103-840A-2     | Sequence 2, Appli  |
| c 20 | 148.4 | 10.3 | 4411529 | 3 | US-09-103-840A-1     | Sequence 1, Appli  |
| 21   | 138.8 | 9.7  | 2664    | 4 | US-09-902-540-8810   | Sequence 8810, Ap  |
| 22   | 138.8 | 9.7  | 8122    | 4 | US-09-902-540-937    | Sequence 937, App  |
| 23   | 133.8 | 9.3  | 1341    | 4 | US-09-710-279-2249   | Sequence 2249, Ap  |
| 24   | 133.8 | 9.3  | 1359    | 3 | US-09-134-001C-1336  | Sequence 1336, Ap  |
| 25   | 133.8 | 9.3  | 3666    | 4 | US-09-710-279-3543   | Sequence 3543, Ap  |
| 26   | 133.8 | 9.3  | 3861    | 4 | US-09-710-279-4124   | Sequence 4124, Ap  |
| 27   | 130.2 | 9.1  | 447     | 4 | US-09-252-991A-16138 | Sequence 16138, A  |
| 28   | 126   | 8.8  | 1347    | 4 | US-09-583-110-2001   | Sequence 2001, Ap  |
| c 29 | 126   | 8.8  | 13425   | 3 | US-08-961-527-151    | Sequence 151, App  |
| 30   | 125.2 | 8.7  | 4259    | 3 | US-09-155-183-12     | Sequence 12, Appli |
| 31   | 125.2 | 8.7  | 4259    | 4 | US-09-733-383-12     | Sequence 12, Appli |
| c 32 | 124.2 | 8.7  | 1425    | 4 | US-09-252-991A-10987 | Sequence 10987, A  |
| 33   | 124.2 | 8.7  | 1470    | 4 | US-09-252-991A-11262 | Sequence 11262, A  |
| 34   | 116.6 | 8.1  | 1350    | 4 | US-09-252-991A-1330  | Sequence 1330, Ap  |
| 35   | 116.6 | 8.1  | 2538    | 4 | US-09-252-991A-1285  | Sequence 1285, Ap  |
| c 36 | 116.6 | 8.1  | 2571    | 4 | US-09-252-991A-1279  | Sequence 1279, Ap  |
| 37   | 114.6 | 8.0  | 576     | 4 | US-09-252-991A-11196 | Sequence 11196, A  |
| 38   | 97.6  | 6.8  | 1347    | 4 | US-09-252-991A-10926 | Sequence 10926, A  |
| 39   | 97.6  | 6.8  | 1395    | 4 | US-09-252-991A-10988 | Sequence 10988, A  |
| 40   | 92.2  | 6.4  | 726     | 4 | US-09-134-000C-1562  | Sequence 1562, Ap  |
| 41   | 91.4  | 6.4  | 1269    | 4 | US-09-902-540-2402   | Sequence 2402, Ap  |
| 42   | 91.4  | 6.4  | 16782   | 4 | US-09-902-540-1105   | Sequence 1105, Ap  |
| 43   | 89.6  | 6.2  | 1359    | 4 | US-09-252-991A-11454 | Sequence 11454, A  |
| 44   | 89.6  | 6.2  | 1395    | 4 | US-09-252-991A-11477 | Sequence 11477, A  |
| c 45 | 89.6  | 6.2  | 1452    | 4 | US-09-252-991A-11417 | Sequence 11417, A  |

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 18:14:46 ; Search time 987 Seconds  
(without alignments)  
9217.496 Million cell updates/sec

Title: US-10-790-224A-19

Perfect score: 1434

Sequence: 1 gtggcgttgaaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Result<br>No. | Score  | Query |         |         |                      |                      | Description        |
|---------------|--------|-------|---------|---------|----------------------|----------------------|--------------------|
|               |        | Match | Length  | DB      | ID                   |                      |                    |
| 1             | 1434   | 100.0 | 1434    | 21      | US-10-790-224A-19    |                      | Sequence 19, Appl  |
| 2             | 1434   | 100.0 | 2500    | 19      | US-10-720-177-3      |                      | Sequence 3, Appli  |
| 3             | 1424.4 | 99.3  | 3309400 | 9       | US-09-738-626-1      |                      | Sequence 1, Appli  |
| 4             | 1421.4 | 99.1  | 1431    | 9       | US-09-738-626-3485   |                      | Sequence 3485, Ap  |
| 5             | 933.2  | 65.1  | 1434    | 17      | US-10-282-122A-17591 |                      | Sequence 17591, A  |
| 6             | 705.8  | 49.2  | 1437    | 20      | US-10-695-155-93     |                      | Sequence 93, Appl  |
| 7             | 705.8  | 49.2  | 38110   | 20      | US-10-475-024-24     |                      | Sequence 24, Appl  |
| 8             | 705.8  | 49.2  | 38110   | 22      | US-10-475-026-24     |                      | Sequence 24, Appl  |
| 9             | 693.2  | 48.3  | 2256646 | 19      | US-10-470-565-1      |                      | Sequence 1, Appli  |
| c             | 10     | 663.2 | 46.2    | 9025608 | 15                   | US-10-156-761-1      | Sequence 1, Appli  |
|               | 11     | 660.4 | 46.1    | 1407    | 15                   | US-10-156-761-5982   | Sequence 5982, Ap  |
|               | 12     | 483.8 | 33.7    | 1410    | 9                    | US-09-815-242-7990   | Sequence 7990, Ap  |
|               | 13     | 483.8 | 33.7    | 1410    | 17                   | US-10-282-122A-30603 | Sequence 30603, A  |
|               | 14     | 460.2 | 32.1    | 1497    | 17                   | US-10-282-122A-15130 | Sequence 15130, A  |
|               | 15     | 458.8 | 32.0    | 1404    | 17                   | US-10-282-122A-31763 | Sequence 31763, A  |
|               | 16     | 456   | 31.8    | 1413    | 17                   | US-10-282-122A-11289 | Sequence 11289, A  |
|               | 17     | 449.6 | 31.4    | 1413    | 17                   | US-10-282-122A-13799 | Sequence 13799, A  |
|               | 18     | 446.2 | 31.1    | 1407    | 17                   | US-10-282-122A-19817 | Sequence 19817, A  |
|               | 19     | 440.8 | 30.7    | 1017    | 22                   | US-10-755-415-117    | Sequence 117, App  |
| c             | 20     | 434.8 | 30.3    | 1404    | 17                   | US-10-282-122A-33381 | Sequence 33381, A  |
|               | 21     | 423.6 | 29.5    | 1410    | 17                   | US-10-282-122A-41379 | Sequence 41379, A  |
|               | 22     | 419   | 29.2    | 1407    | 17                   | US-10-282-122A-23289 | Sequence 23289, A  |
|               | 23     | 398   | 27.8    | 1410    | 17                   | US-10-282-122A-41832 | Sequence 41832, A  |
|               | 24     | 392   | 27.3    | 1344    | 17                   | US-10-282-122A-13000 | Sequence 13000, A  |
|               | 25     | 391.8 | 27.3    | 1410    | 9                    | US-09-815-242-6321   | Sequence 6321, Ap  |
|               | 26     | 391.8 | 27.3    | 1410    | 15                   | US-10-299-799-2      | Sequence 2, Appli  |
|               | 27     | 391.8 | 27.3    | 1410    | 17                   | US-10-282-122A-20584 | Sequence 20584, A  |
|               | 28     | 391.8 | 27.3    | 1410    | 18                   | US-10-612-779-88     | Sequence 88, Appl  |
|               | 29     | 391.2 | 27.3    | 1410    | 9                    | US-09-815-242-9691   | Sequence 9691, Ap  |
| c             | 30     | 391.2 | 27.3    | 1410    | 17                   | US-10-282-122A-39876 | Sequence 39876, A  |
|               | 31     | 382.2 | 26.7    | 1419    | 17                   | US-10-282-122A-29891 | Sequence 29891, A  |
|               | 32     | 375   | 26.2    | 1409    | 17                   | US-10-282-122A-37301 | Sequence 37301, A  |
|               | 33     | 374.8 | 26.1    | 1533    | 17                   | US-10-282-122A-28986 | Sequence 28986, A  |
|               | 34     | 338.2 | 23.6    | 1413    | 17                   | US-10-282-122A-8418  | Sequence 8418, Ap  |
|               | 35     | 336.8 | 23.5    | 2731748 | 19                   | US-10-297-465A-1     | Sequence 1, Appli  |
|               | 36     | 292.2 | 20.4    | 1407    | 17                   | US-10-282-122A-32655 | Sequence 32655, A  |
|               | 37     | 286.4 | 20.0    | 1419    | 17                   | US-10-282-122A-31024 | Sequence 31024, A  |
|               | 38     | 277.6 | 19.4    | 1419    | 9                    | US-09-815-242-7040   | Sequence 7040, Ap  |
|               | 39     | 277.6 | 19.4    | 1419    | 17                   | US-10-282-122A-22148 | Sequence 22148, A  |
| c             | 40     | 277.6 | 19.4    | 1830121 | 17                   | US-10-329-670-1      | Sequence 1, Appli  |
|               | 41     | 277.6 | 19.4    | 1830121 | 20                   | US-10-158-865-1      | Sequence 1, Appli  |
|               | 42     | 277.6 | 19.4    | 1830121 | 22                   | US-10-981-687-1      | Sequence 1, Appli  |
|               | 43     | 277.2 | 19.3    | 1407    | 17                   | US-10-282-122A-25145 | Sequence 25145, A  |
|               | 44     | 244.2 | 17.0    | 1407    | 17                   | US-10-282-122A-26893 | Sequence 26893, A  |
|               | 45     | 244.2 | 17.0    | 65792   | 18                   | US-10-672-787-31     | Sequence 31, Appli |

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 11:32:21 ; Search time 5114 Seconds  
(without alignments)  
10673.477 Million cell updates/sec

Title: US-10-790-224A-19

Perfect score: 1434

Sequence: 1 gtggcggttgaaccccgga.....aattgtacttcgactgctaa 1434

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_htc:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result | Query | %     | No.  | Score | Match | Length   | DB                 | ID       | Description        |
|--------|-------|-------|------|-------|-------|----------|--------------------|----------|--------------------|
|        |       |       | 1    | 246.6 | 17.2  | 1188     | 9                  | CG745336 | CG745336 P038-1-H0 |
|        |       |       | 2    | 243.4 | 17.0  | 1069     | 8                  | BZ548371 | BZ548371 pacsl-60  |
| c      | 3     | 191.2 | 13.3 | 840   | 9     | CG146861 | CG146861 PUIME33TD |          |                    |
| c      | 4     | 176   | 12.3 | 478   | 1     | AL587125 | AL587125 AL587125  |          |                    |
| c      | 5     | 166   | 11.6 | 762   | 9     | CG128373 | CG128373 PUIFH05TD |          |                    |
| c      | 6     | 166   | 11.6 | 851   | 8     | CC381873 | CC381873 PUHFA22TD |          |                    |
| c      | 7     | 164   | 11.4 | 814   | 9     | CL683966 | CL683966 PRI0138b  |          |                    |
| c      | 8     | 161.6 | 11.3 | 825   | 8     | CC443184 | CC443184 PUHHO69TD |          |                    |
| c      | 9     | 161.6 | 11.3 | 850   | 8     | BZ701245 | BZ701245 PUBMN15TD |          |                    |

|      |       |      |      |   |           |                    |
|------|-------|------|------|---|-----------|--------------------|
| 10   | 159   | 11.1 | 488  | 7 | CF606601  | CF606601 FOGLI02_0 |
| c 11 | 157.6 | 11.0 | 863  | 8 | BZ574029  | BZ574029 msh2_3475 |
| 12   | 151.4 | 10.6 | 598  | 9 | CG126167  | CG126167 PUIFQ05TB |
| c 13 | 149.4 | 10.4 | 1236 | 8 | BZ555775  | BZ555775 pacs1-60_ |
| c 14 | 144.6 | 10.1 | 1354 | 8 | BZ548975  | BZ548975 pacs1-60_ |
| 15   | 143.4 | 10.0 | 883  | 8 | CC439227  | CC439227 PUHMO46TB |
| c 16 | 141.6 | 9.9  | 815  | 8 | BZ705035  | BZ705035 PUBMO84TD |
| 17   | 138.4 | 9.7  | 567  | 7 | CF943093  | CF943093 NcESTqab9 |
| c 18 | 137.8 | 9.6  | 699  | 8 | BZ684738  | BZ684738 PUBFS60TD |
| c 19 | 130.2 | 9.1  | 799  | 9 | CG110558  | CG110558 PUIIA51TD |
| c 20 | 130.2 | 9.1  | 844  | 9 | CG128001  | CG128001 PUILH94TD |
| c 21 | 130.2 | 9.1  | 850  | 8 | BZ704494  | BZ704494 PUBMJ14TD |
| 22   | 130.2 | 9.1  | 901  | 8 | CC435159  | CC435159 PUHDF85TB |
| c 23 | 130.2 | 9.1  | 902  | 8 | CC435165  | CC435165 PUHDF85TD |
| c 24 | 130.2 | 9.1  | 944  | 8 | BZ679052  | BZ679052 PUBGZ43TD |
| c 25 | 130.2 | 9.1  | 1017 | 9 | CG130318  | CG130318 PUIFB78TD |
| 26   | 130   | 9.1  | 525  | 9 | TSP458769 | AJ458769 Thermotog |
| 27   | 123.4 | 8.6  | 320  | 6 | CB821337  | CB821337 EST 2188  |
| 28   | 120.2 | 8.4  | 726  | 9 | CG137357  | CG137357 PUIHH87TB |
| 29   | 120.2 | 8.4  | 1138 | 2 | BE636680  | BE636680 rockefell |
| 30   | 117.2 | 8.2  | 910  | 8 | CC381870  | CC381870 PUHFA22TB |
| c 31 | 115.2 | 8.0  | 422  | 9 | CG458779  | CG458779 PUILB34TD |
| c 32 | 110.2 | 7.7  | 533  | 8 | BZ296095  | BZ296095 CG1855.f1 |
| c 33 | 106.6 | 7.4  | 682  | 8 | BZ668122  | BZ668122 PUBCR86TD |
| c 34 | 106   | 7.4  | 954  | 8 | BZ668332  | BZ668332 PUBEZ18TD |
| c 35 | 102.8 | 7.2  | 382  | 9 | CG107402  | CG107402 PUILV62TD |
| 36   | 101.4 | 7.1  | 502  | 4 | BM176045  | BM176045 TgESTzyb2 |
| 37   | 100.2 | 7.0  | 818  | 8 | BZ687214  | BZ687214 PUBDI18TD |
| c 38 | 96.8  | 6.8  | 481  | 8 | AZ049103  | AZ049103 GSSBru050 |
| 39   | 96    | 6.7  | 540  | 8 | BZ894864  | BZ894864 Hg4_0154  |
| c 40 | 91.6  | 6.4  | 786  | 8 | CC377190  | CC377190 PUHKI89TD |
| c 41 | 91.6  | 6.4  | 932  | 9 | CG455027  | CG455027 PUIJY83TD |
| c 42 | 89.4  | 6.2  | 1176 | 8 | BZ569521  | BZ569521 pacs2-164 |
| 43   | 87.6  | 6.1  | 535  | 1 | AL921359  | AL921359 AL921359  |
| c 44 | 78.2  | 5.5  | 1124 | 8 | BZ558114  | BZ558114 pacs1-60_ |
| 45   | 77    | 5.4  | 255  | 8 | BZ705385  | BZ705385 PUBMJ94TD |